Author index

Albersheim, P. *see* Augur, C.
Albrecht, H. *see* Goldsbrough, A.P.
Allen, R.L. and Lonsdale, D.M. *Molecular characterization of one of the maize polygalacturonase gene family members which are expressed during late pollen development* 261
Andrawis, A., Solomon, M. and Delmer, D.P. *Cotton fiber annexins: a potential role in the regulation of callose synthase* 763
Apel, K. *see* Bohl, S.
Araki, T. and Komeda, Y. *Analysis of the role of the late-flowering locus,* Gl, *in the flowering of* Arabidopsis thaliana 231
Arrowsmith, D.A. *see* de Silva, J.
Augur, C., Benhamou, N., Darvill, A. and Albersheim, P. *Purification, characterization, and cell wall localization of an α-fucoside that inactivates a xyloglucan oligosaccharin* 415
Avila, J., Nieto, C., Canas, L., Benito, M.J. and Paz-Ares, J. Petunia hybrida *genes related to the maize regulatory* C1 *gene and to animal* myb *proto-oncogenes* 553

Bachmair, A. *see* Becker, F.
Bade, J. *see* Koornneef, M.
Barton, S.L. *see* Picton, S.
Bäumlein, H. *see* Macas, J.
Becker, F., Buschfeld, E., Schell, J. and Bachmair, A. *Altered response to viral infection by tobacco plants perturbed in ubiquitin system* 875
Becker, W.M. *see* Sloan, J.S.
Bell, P.J. *see* Wright, S.Y.
Benhamou, N. *see* Augur, C.
Benito, M.J. *see* Avila, J.
Benner, M.S. *see* Schickler, H.
Bevan, M. *see* Shufflebottom, D.
Bird, C.R. *see* Hall, L.N.
Bisseling, T. *see* Lauridsen, P.
Bisseling, T. *see* Wang, W.-C.
Blundell, R.P. *see* Roberts, M.R.
Bogorad, L. *see* Salvador, M.L.
Bögre, L. *see* Páy, A.
Bögre, L. *see* Jonak, C.
Bohl, S. and Apel, K. *A novel fingerprint method for analyzing the expression of complex multigene families of very low transcript abundance* 887
Bol, J.F. *see* van de Rhee, M.D.
Boniwell, J.M. *see* Hall, L.N.
Bonnett, H.T., Djurberg, I., Fajardo, M. and Glimelius, K. *A mutation causing variegation and abnormal development in tobacco is associated with an altered mitochondrial DNA* 519
Botterman, J. *see* de Oliveira, D.E.
Bouzayen, M. *see* Picton, S.
Bowsher, C.G., Hucklesby, D.P. and Emes, M.J. *Induction of ferredoxin-NADP$^+$ oxidoreductase and ferredoxin synthesis in pea root plastids during nitrate assimilation* 463
Bressan, R.A. *see* Zhu, J.-K.
Bundick, Y. *see* Hall, L.N.
Buschfeld, E. *see* Becker, F.

Cai, D., Herrmann, R.G. and Klösgen, R.B. *The 20 kDa apoprotein of the CP24 complex of photosystem II: an alternative model to study import and intra-organellar routing of nuclear-encoded thylakoid proteins* 383
Canas, L. *see* Avila, J.
Cardon, G.H., Frey, M., Saedler, H. and Gierl, A. *Mobility of the maize transposable element* En/Spm *in* Arabidopsis thaliana 773
Carmona, M.J., Molina, A., Fernández, J.A., López-Fando, J.J. and Garciá-Olmedo, F. *Expression of the α-thionin gene from barley in tobacco confers enhanced resistance to bacterial pathogens* 457
Carneiro, M. and Vilaine, F. *Differential expression of the* rol*A plant oncogene and its effect on tobacco development* 785
Carpenter, B. *see* Girod, P.-A.
Carpita, N.C. and Gibeaut, D.M. *Structural models of primary cell walls in flowering plants: consistency of molecular structure with the physical properties of the walls during growth* 1
Carpita, N.C. *see* Zhu, J.-K.
Carrayol, E. *see* Marsolier, M.-C.
Carroll, B.J. *see* Klimyuk, V.I.
Cartinhour, S. *see* Hauge, B.M.
Caspar, T. and Quail, P.H. *Promoter and leader regions involved in the expression of the* Arabidopsis *ferredoxin A gene* 161
Chang, C. *see* Hauge, B.M.
Charpenteau, M. *see* Vidal, V.
Chengappa, S. *see* de Silva, J.
Cherry, J.M. *see* Hauge, B.M.
Cheung, A.Y., May, B., Kawata, E.E., Gu, Q. and Wu, H.-M. *Characterization of cDNAs for stylar transmitting tissue-specific proline-rich proteins in tobacco* 151
Chua, N.-H. *see* Liu, C.-M.
Collinge, D.B., Kragh, K.M., Mikkelsen, J.D., Nielsen, K.K., Rasmussen, U. and Vad, K. *Plant chitinases* 31
Coppieters, J. *see* de Oliveira, D.E.
Cove, D.J. *see* Leech, M.J.
Cove, D.J. *Mutant analysis, a key tool for the study of metabolism and development* 303
Crozier, A. *see* Nilsson, O.

Darvill, A. *see* Augur, C.
de Oliveira, D.E., Franco, L.O., Simoens, C., Seurinck, J., Coppieters, J., Botterman, J. and Van Montagu, M. *Inflorescence-specific genes from* Arabidopsis thaliana *encoding glycine-rich proteins* 495
de Silva, J., Jarman, C.D., Arrowsmith, D.A., Stronach, M.S., Chengappa, S., Sidebottom, C. and Reid, J.S.G. *Molecular characterization of a xyloglucan-specific* endo-(*1→4*)-β-*D glucanase) from nasturtium seeds* 701
de Vries, F. *see* Wang, W.-C.
Delmer, D.P. *see* Andrawis, A.
Dennis, E.S. *see* Foley, R.C.
Dillenschneider, M. *see* Vidal, V.
Ding, J.P. and Pickard, B.G. *Mechanosensory calcium-selective cation channels in epidermal cells* 83
Ding, J.P. and Pickard, B.G. *Modulation of mechanosensitive calcium-selective cation channels by temperature* 713
Dix, P.J. *see* O'Neill, C.
Dix, P.J. *The role of mutant cell lines in studies on environmental stress tolerance: an assessment* 309

Dixon, R.A. *see* Yua, L.M.
Djurberg, I. *see* Bonnett, H.T.
Doerner, P.W. *see* Zhu, Q.
Draper, J. *see* Roberts, M.R.
Draper, J. *see* Warner, S.A.J.
Dure III, L. *A repeating 11-mer amino acid motif and plant dessication* 363
Düring, K., Porsch, P., Fladung, M. and Lörz, H. *Transgenic potato plants resistant to the phytopathogenic bacterium* Erwinia carotovora 587

Edwards, K. *see* Shufflebottom, D.
Ellis. J.G. *see* Foley, R.C.
Emes, M.J. *see* Bowsher, C.G.
Esquerré-Tugayé, M.-T. *see* Fournier, J.

Fajardo, M. *see* Bonnett, H.T.
Fanutti, C., Gidley, M.J. and Reid, J.S.G. *Action of a pure xyloglucan* endo-*transglycosylase (formerly called xyloglucan-specific* endo-(*1→4*)-β-D-*glucanase) from the cotyledons of germinated nasturtium seeds* 691
Fedoroff, N.V. and Smith, D.L. *A versatile system for detecting transposition in* Arabidopsis 273
Fellous, A. *see* Schellenbaum, P.
Fernandez, J.A. *see* Carmona, M.J.
Fladung, M. *see* Düring, K.
Fladung, M. *see* Schmülling, T.
Fletcher, J.D. *see* Hall. L.N.
Foley, R.C., Grossman, C., Ellis, J.G., Llewellyn, D.J., Dennis, E.S., Peacock, W.J. and Singh, K.B. *Isolation of a maize bZIP protein subfamily: candidates for the ocs-element transcription factor* 669
Foster, G.D. *see* Roberts, M.R.
Fournier, J., Pouénat, M.-L., Rickauer, M., Rabinovitch-Chable, H., Rigaud, M. and Esquerré-Tugayé, M.-T. *Purification and characterization of elicitor-induced lipoxygenase in tobacco cells* 63
Franco, L.O. *see* de Oliveira, D.E.
Franssen, H. *see* Lauridsen, P.
Franssen, H. *see* Wang, W.-C.
Frey, M. *see* Cardon, G.H.

Galili, G. *see* Karchi, H.
Garcia-Olmedo, F. *see* Carmona, M.J.
Gibeaut, D.M. *see* Carpita, N.C.
Gidley, M.J. *see* Fanutti, C.
Gierl, A. *see* Cardon, G.H.
Girod, P.-A., Carpenter, B., van Nocker, S., Sullivan, M.L. and Vierstra, R.D. *Homologs of the essential ubiquitin conjugating enzymes UBC1, 4, and 5 in yeast are encoded by a multigene family in* Arabidopsis thaliana 545
Glimelius, K. *see* Bonnett, H.T.
Goldsbrough, A.P., Albrecht, H., and Stratford, R. *Salicylic acid-inducible binding of a tobacco nuclear protein to a 10 bp sequence which is highly conserved amongst stress-inducible genes* 563
Goodman, H.M. *see* Hauge, B.M.
Goodman, H.M. *see* Lazar, G.
Görg, R., Hollricher, K. and Schulze-Lefert, P. *Functional analysis and RFLP-mediated mapping of the* Mlg *resistance locus in barley* 857
Gotor, C., Romero, L.C., Inouye, K. and Lam, E. *Analysis of three tissue-specific elements from the wheat* Cab-1 *enhancer* 509
Gray, J.C. *see* Pwee, K.-H.
Greenland, A.J. *see* Wright, S.Y.
Grierson, D. *see* Hall, L.N.
Grierson, D. *see* Picton, S.
Grossman, C. *see* Foley, R.C.
Grossman, K. *see* Schmülling, T.
Gu, Q. *see* Cheung, A.Y.
Guan, L. and Scandalios, J.G. *Characterization of the catalase antioxidant defense gene* Cat1 *of maize, and its developmentally regulated expression in transgenic tobacco* 527

Hall, L.N., Tucker, G.A., Smith, C.J.S., Watson, C.F., Seymour, G.B., Bundick, Y., Boniwell, J.M., Fletcher, J.D., Ray, J.A., Schuch, W., Bird, C.R. and Grierson, D. *Antisense inhibition of pectin esterase gene expression in transgenic tomatoes* 121
Hamilton, A.J. *see* Picton, S.
Hanhart, C. *see* Koornneef, M.
Hanley, S.M. *see* Hauge, B.M.
Hasegawa, P.M. *see* Zhu, J.-K.
Hauge, B.M., Hanley, S.M., Cartinhour, S., Cherry, J.M., Goodman, H.M., Koornneef, M., Stam, P., Chang, C., Kempin, S., Medrano, L. and Meyerowitz, E.M. *An integrated genetic/RFLP map of the* Arabidopsis thaliana *genome* 745
Heberle-Bors, E. *see* Páy, A.
Heberle-Bors, E. *see* Jonak, C.
Hendriks, P. *see* Wang, W.-C.
Herrmann, R.G. *see* Cai, D.
Hirel, B. *see* Marsolier, M.-C.
Hirt, H. *see* Páy, A.
Hirt, H. *see* Jonak, C.
Hodge, R. *see* Roberts, M.R.
Hofmann, B. *see* Krapp, A.
Hollricher, K. *see* Görg, R.
Horsman, K. *see* Koornneef, M.
Horváth, E. *see* O'Neill, C.
Horváth, G.V. *see* O'Neill, C.
Houben, A. *see* Macas, J.
Hucklesby, D.P. *see* Bowsher, C.G.

Inouye, K. *see* Gotor, C.
Iwabuchi, M. *see* Terada, R.

Jarman, C.D. *see* de Silva, J.
Jonak, C. *see* Páy, A.
Jonak, C., Pay, A., Bögre, L., Hirt, H., and Heberle-Bors, E. *The plant homologue of MAP kinase is expressed in a cell cycle-dependent and organ-specific manner* 611
Jones, J.D.G. *see* Klimyuk, V.I.

Kammerer, W. *see* Leech, M.J.
Kaneko, Y. *see* Thoma, S.
Karchi, H., Shaul, O. and Galili, G. *Seed-specific expression of a bacterial desensitized aspartate kinase increases the production of seed threonine and methionine in transgenic tobacco* 721
Katinakis, P. *see* Wang, W.-C.
Kawata, E.E. *see* Cheung, A.Y.
Kempin, S. *see* Hauge, B.M.
Kitano, H., Tamura, Y., Satoh, H. and Nagato, Y. Hierarchical regulation of organ differentiation during embryogenesis in rice 607

Klein, U. *see* Salvador, M.L.
Klimyuk, V.I., Carroll, B.J., Thomas, C.M. and Jones, J.D.G. *Alkali treatment for rapid preparation of plant material for reliable PCR analysis* 493
Klösgen, R.B. *see* Cai, D.
Kolattukudy, P.E. *see* Sherf, B.A.
Komeda, Y. *see* Araki, T.
Koornneef, M. *see* Hauge, B.M.
Koornneef, M., Bade, J., Hanhart, C., Horsman, K., Schel, J., Soppe, W., Verkerk, R. and Zabel, P. *Characterization and mapping of a gene controlling shoot regeneration in tomato* 131
Kragh, K.M. *see* Collinge, D.D.
Krapp, A., Hofmann, B., Schäfer, C. and Stitt, M. *Regulation of the expression of* rbcS *and other photosynthetic genes by carbohydrates: a mechanism for the 'sink regulation' of photosynthesis?* 817
Kumar, A. *see* Roberts, M.R.

Lam, E. *see* Gotor, C.
Lamb, C.J. *see* Yua, L.M.
Lamb, C.J. *see* Zhu, Q.
Lambert, A.-M. *see* Schellenbaum, P.
Lauridsen, P., Franssen, H., Stougaard, J., Bisseling, T. and Marcker, K.A. *Conserved regulation of the soybean early nodulin* ENOD2 *gene promoter in determinate and indeterminate transgenic root nodules* 483
Lazar, G., Zhang, H. and Goodman, H.M. *The origin of the bifunctional dihydrofolate reductase–thymidylate synthase isogenes of* Arabidopsis thaliana 657
Lee, N.-G., Stein, B., Suzuki, H. and Verma, D.P.S. *Expression of antisense nodulin-35 RNA in* Vigna aconitifolia *transgenic root nodules retards peroxisome development and affects nitrogen availability to the plant* 599
Leech, M.J., Kammerer, W., Cove, D.J., Martin, C. and Wang, T.L. *Expression of* myb*-related genes in the moss,* Physcomitrella patens 51
Link, G. *see* Nickelsen, J.
Liu, C.-M., Xu, Z.-H. and Chua, N.-H. *Proembryo culture:* in vitro *development of early globular-stage zygotic embryos from* Brassica juncea 291
Llewellyn, D.J. *see* Foley, R.C.
Lonsdale, D.M. *see* Allen, R.L.
Lopez-Fando, J.J. *see* Carmona, M.J.
Lörz. H. *see* Düring, K.
Lou, H., McCullough, A.J. and Schuler, M.A. *Expression of maize* Adh1 *intron mutants in tobacco nuclei* 393

Macas, J., Weschke, W., Bäumlein, H., Pich, U., Houben, A., Wobus, U. and Schubert, I. *Localization of vicilin genes via polymerase chain reaction on microisolated field bean chromosomes* 883
Mairinger, T. *see* Páy, A.
Marcker, K.A. *see* Lauridsen, P.
Marsolier, M.-C., Carrayol, E. and Hirel, B. *Multiple functions of promoter sequences involved in organ-specific expression and ammonia regulation of a cytosolic soybean glutamine synthetase gene in transgenic* Lotus corniculatus 405
Martin, C. *see* Leech, M.J.
Martin, C. *The use of mutants to study plant metabolism and development* 301
May, B. *see* Cheung, A.Y.
McCullough, A.J. *see* Lou, H.
Medberry, S.L. and Olszewski, N.E. *Identification of* cis *elements involved in Commelina yellow mottle virus promoter activity* 619
Medgyesy, P. *see* O'Neill, C.
Medrano, L. *see* Hauge, B.M.
Meskiene, I. *see* Páy, A.
Messing, J. *see* Schickler, H.
Meyerowitz, E.M. *see* Hauge, B.M.
Mikkelsen, J.D. *see* Collinge, D.D.
Molina, A. *see* Carmona, M.J.
Murphy, D.J. *see* Roberts, M.R.

Nagato, Y. *see* Kitano, H.
Nakayama, T. *see* Terada, R.
Nickelsen, J. and Link, G. *The 54 kDa RNA-binding protein from mustard chloroplasts mediates endonucleolytic transcript 3' end formation* in vitro 537
Nielsen, K.K. *see* Collinge, D.D.
Nieto, C. *see* Avila, J.
Nilsson, O., Crozier, A., Schmülling, T., Sandberg, G. and Olsson, O. *Indole-3-acetic acid homeostasis in transgenic tobacco plants expressing the* Agrobacterium rhizogenes rolB *gene* 681

O'Neill, C., Horváth, G.V., Horváth, E., Dix, P.J. and Medgyesy, P. *Chloroplast transformation in plants: polyethylene glycol (PEG) treatment of protoplasts is an alternative to biolistic delivery systems* 729
Olsson, O. *see* Nilsson, O.
Olszewski, N.E. *see* Medberry, S.L.

Páy, A. *see* Jonak, C.
Páy, A., Jonak, C., Bögre, L., Meskiene, I., Mairinger, T., Szalay, A., Heberle-Bors, E. and Hirt, H. *The* MsK *family of alfalfa protein kinase genes encodes homologues of* shaggy/glycogen synthase kinase-3 *and shows differential expression patterns in plant organs* 847
Paz-Ares, J. *see* Avila, J.
Peacock, W.J. *see* Foley, R.C.
Peter, C. *see* Schellenbaum, P.
Pich, U. *see* Macas, J.
Pickard, B.G. *see* Ding, J.P.
Picton, S., Barton, S.L., Bouzayen, M., Hamilton, A.J. and Grierson, D. *Altered fruit ripening and leaf senescence in tomatoes expressing an antisense ethylene-forming enzyme transgene* 469
Porsch, P. *see* Düring, K.
Pouénat, M.-L. *see* Fournier, J.
Pwee, K.-H. and Gray, J.C. *The pea plastocyanin promoter directs cell-specific but not full light-regulated expression in transgenic tobacco plants* 437

Quail, P.H. *see* Caspar, T.

Rabinovitch-Chable, H. *see* Fournier, R.
Ranjeva, R. *see* Vidal, V.
Ranty, B. *see* Vidal, V.
Rasmussen, U. *see* Collinge, D.D.
Ray, J.A. *see* Hall, L.N.
Reid, J.S.G. *see* Fanutti, C.
Reid, J.S.G. *see* de Silva, J.
Ribeiro-Neto, L. *see* Sheahan, J.J.
Rickauer, M. *see* Fournier, J.
Rigaud, M. *see* Fournier, J.
Roberts, M.R., Foster, G.D., Blundell, R.P., Robinson, S.W.,

Kumar, A., Draper, J. and Scott, R. *Gametophytic and sporophytic expression of an anther-specific* Arabidopsis thaliana *gene* 111
Roberts, M.R., Hodge, R., Ross, J.H.E., Sorensen, A., Murphy, D.J., Draper, J. and Scott, R. *Characterization of a new class of oleosins suggests a male gametophyte-specific lipid storage pathway* 629
Robinson, S.W. *see* Roberts, M.R.
Romero, L.C. *see* Gotor, C.
Ross, J.H.E. *see* Roberts, M.R.

Saedler, H. *see* Cardon, G.H.
Salvador, M.L., Klein, U. and Bogorad, L. *Light-regulated and endogenous fluctuations of chloroplast transcript levels in* Chlamydomonas. *Regulation by transcription and RNA degradation* 213
Sandberg, G. *see* Nilsson, O.
Satoh, H. *see* Kitano, H.
Scandalios, J.G. *see* Guan, L.
Schäfer, C. *see* Krapp, A.
Schel, J. *see* Koornneef, M.
Schell, J. *see* Becker, F.
Schell, J. *see* Schmülling, T.
Schellenbaum, P., Vantard, M., Peter, C., Fellous, A. and Lambert, A.-M. *Co-assembly properties of higher plant microtubule-associated proteins with purified brain and plant tubulins* 253
Schickler, H., Benner, M.S. and Messing, J. *Repression of the high-methionine zein gene in the maize inbred line Mo17* 221
Schmülling, T. *see* Nilsson, O.
Schmulling, T., Fladung, M., Grossman, K. and Schell, J. *Hormonal content and sensitivity of transgenic tobacco and potato plants expressing single* rol *genes of* Agrobacterium rhizogenes *T-DNA* 371
Schubert, I. *see* Macas, J.
Schuch, W. *see* Shufflebottom, D.
Schuch, W. *see* Hall, L.N.
Schuler, M.A. *see* Lou, H.
Schulze-Lefert, P. *see* Görg, R.
Schwartz, B.W. *see* Sloan, J.S.
Scott, R. *see* Roberts, M.R.
Scott, R. *see* Warner, S.A.J.
Seurinck, J. *see* de Oliveira, D.E.
Seymour, G.B. *see* Hall, L.N.
Shaul, O. *see* Karchi, H.
Sheahan, J.J., Ribeiro-Neto, L. and Suissman, M.R. *Cesium-insensitive mutants of* Arabidopsis thaliana 647
Sherf, B.A. and Kolattukudy, P.E. *Developmentally regulated expression of the wound- and pathogen-responsive tomato anionic peroxidase in green fruits* 829
Shi, J. *see* Zhu, J.-K.
Shimamoto, K. *see* Terada, R.
Shufflebottom, D., Edwards, K., Schuch, W. and Bevan, M. *Transcription of two members of a gene family encoding phenylalanine ammonia-lyase leads to remarkably different cell specificities and induction patterns* 835
Sidebottom, C. *see* de Silva, J.
Simoens, C. *see* de Olivera, D.E.
Singh, K.B. *see* Foley, R.C.
Singh, U. *see* Zhu, J.-K.
Sloan, J.S., Schwartz, B.W. and Becker, W.M. *Promoter analysis of a light-regulated gene encoding hydroxypyruvate reductase, an enzyme of the photorespiratory glycolate pathway* 867
Smeekens, S. *see* Vorst, O.
Smith, C.J.S. *see* Hall, L.N.
Smith, D.L. *see* Fedoroff, N.V.
Smolders, A. *see* Wang, W.-C.
Solomon, M. *see* Andrawis, A.
Somerville, C. *see* Thoma, S.
Soppe, W. *see* Koornneef, M.
Sorensen, A. *see* Roberts, M.R.
Spree, J. *see* Wang, W.-C.
Stam, P. *see* Hauge, B.M.
Stam, P. *Construction of integrated genetic linkage maps by means of a new computer package*: JoinMap 739
Stein, B. *see* Lee, N.-G.
Stitt, M. *see* Krapp, A.
Stougaard, J. *see* Lauridsen, P.
Stougaard, J. *Substrate-dependent negative selection in plants using a bacterial cytosine deaminase gene* 755
Stratford, R. *see* Goldsbrough, A.P.
Stronach, M.S. *see* de Silva, J.
Sullivan, M.L. *see* Girod, P.-A.
Suner, M.-M. *see* Wright, S.Y.
Sussman, M.R. *see* Sheahan, J.J.
Suzuki, H. *see* Lee, N.-G.
Szalay, A. *see* Páy, A.

Tamura, Y. *see* Kitano, H.
Terada, R., Nakayama, T., Iwabuchi, M. and Shimamoto, K. *A wheat histone H3 promoter confers division-dependent and -independent expression of the* gus A *gene in transgenic rice plants* 241
Thoma, S., Kaneko, Y. and Somerville, C. *A non-specific lipid transfer protein from* Arabidopsis *is a cell wall protein* 427
Thomas, C.M. *see* Klimyuk, V.I.
Tucker, G.A. *see* Hall, L.N.

Vad, K. *see* Collinge, D.D.
van Dam, F. *see* Vorst, O.
van de Rhee, M.D. and Bol, J.F. *Induction of the tobacco* PR-1a *gene by virus infection and salicylate treatment involves an interaction between multiple regulatory elements* 71
van Kammen, A. *see* Wang, W.-C.
Van Montagu, M. *see* de Oliveira, D.E.
van Nocker, S. *see* Girod, P.-A.
Vantard, M. *see* Schellenbaum, P.
Vaudin, M. *see* Wright, S.Y.
Verkerk, R. *see* Koornneef, M.
Verma, D.P.S. *see* Lee, N.-G.
Vidal, V., Ranty, B., Dillenschneider, M., Charpenteau, M. and Ranjeva, R. *Molecular characterization of a 70 kDa heat-shock protein of bean mitochondria* 143
Vierstra, R.D. *see* Girod, P.-A.
Vilaine, F. *see* Carneiro, M.
Vorst, O., van Dam, F., Weisbeek, P. and Smeekens, S. *Light-regulated expression of the* Arabidopsis thaliana ferredoxin A *gene involves both transcriptional and post-transcriptional processes* 793

Walker, J.C. *Receptor-like protein kinase genes of* Arabidopsis thaliana 451
Wang, T.L. *see* Leech, M.J.
Wang, W.-C., Katinakis, P., Hendriks, P., Smolders, A., deVries, F., Spree, J., van Kammen, A., Bisseling, T. and Franssen, H. *Characterization of* GmENOD40, *a gene showing novel patterns of cell-specific expression during soybean nodule development* 573

Warner, S.A.J., Scott, R. and Draper, J. *Isolation of an asparagus intracellular PR gene (AoPR1) wound-responsive promoter by the inverse polymerase chain reaction and its characterization in transgenic tobacco* 191
Watson, C.F. *see* Hall, L.N.
Weisbeek, P. *see* Vorst, O.
Weschke, W. *see* Macas, J.
Wobus, U. *see* Macas, J.
Wright, S.Y., Suner, M.-M., Bell, P.J., Vaudin, M. and Greenland, A.J. *Isolation and characterization of male flower cDNAs from maize* 41
Wu, H.-M. *see* Cheung, A.Y.
Wyatt, S.E. *see* Zhu, J.-K.

Xu, Z.H. *see* Liu, C.-M.

Yua, L.M., Lamb, C.J. and Dixon, R.A. *Purification and biochemical characterization of proteins which bind to the H-box cis-element implicated in transcriptional activation of plant defense genes* 805

Zabel, P. *see* Koornneef, M.
Zhang, H. *see* Lazar, G.
Zhu, J.-K., Shi, J., Singh, U., Wyatt, S.E., Bressan, R.A., Hasegawa, P.M. and Carpita, N.C. *Enriched vitronectin- and fibronectin-like proteins in NaCl-adapted plant cells and evidence for their involvement in plasma membrane-cell wall adhesion* 637
Zhu, Q., Doerner, P.W. and Lamb, C.J. *Stress induction and development regulation of a rice chitinase promoter in transgenic tobacco* 203

Subject index

AC–DS 273
activation sequence 509
  factor-2 509
activator/dissociation 493
Adh1 393
Agrobacterium 371, 681
  rhizogenes 785
alfalfa 611
Allium cepa 83
11 amino acid motif 363
1-aminocyclopropane-1-carboxylic acid 469
ammonia-stimulation 405
amphiphilic helix 363
anionic peroxidase 829
annexin 763
anther 41
anther-specific 111, 495
  genes 495
anthocyanin 335
antibacterial resistance 587
antisense 51
Arabidopsis 745, 657, 793, 835
  thaliana 231, 273, 495, 545, 647
arabinogalactan 1
aspartate kinase 721
Aspergillus nidulans 303
assembly 383
AT dinucleotides 175
avirulence gene 857

B gene 335
β-glucuronidase 241
B-HLH transcription 335
badnavirus 619
barley 457
bifunctional genes 657
binding factor 669
Brassica
  juncea 291
  napus 629
bZIP 669

Cab 509
calcium 763
  regulation 143
callose 763
  synthase 763
CaMV 35S promoter 619
carbohydrate 817
cDNA 41, 701
cell
  cycle 611
  wall 1, 122, 415, 427, 691, 701
cesium insensitive 647
chalcone synthase 805
chaperone 143
chitinase 203
  sequences 31
chloroplast 183, 383, 437, 793
  gene *rps16* 537
  gene *trnK* 537
  RNA 537
  transcript pools 213
  transcription 213
cis
  analysis 483
  element 619
  regulatory elements 71
coiled coil 363
cold
  acclimation 713
  sensitivity 713
computer 745
cotton fibers 763
CoYMU 619
CP24 383
cuticle 427
cybrid 519
cytological regeneration (of shoot regeneration) 131
cytoplasmic mutation 519
cytosine deaminase codA 755
cytoskeleton 637

defence
  responses 31
  gene activation 805
  proteins 457
development 221
differential gene expression 785, 835
direct transformation 729
DNA
  diagnostics 493
  binding domain 51, 553

embryo 347, 457
embryogenesis 607
En/Spm transposition 773
endo-(1→4)-β-D-glucanase 701
endogenous rhythm 213
endonuclease 537
endosperm development 325
enhancer/promoter trap 273
environmental stress 309
epidermis 427, 713
Erwinia 587
essential amino acids 721
ethyl-*N*-phenylcarbamate 83
ethylene 469, 829
eukaryotic marker and reporter gene 755
extensin 1
extracellular matrix 1, 691

ferredoxin 161, 463, 793
  $NADP^+$ oxidoreductase 463
fingerprinting 493
flavonoid 553
flower 151
flowering 231
fruit ripening 121, 469
fucosidase 415
fungal ontogeny 857

gadolinium 83
gametophyte-specific 629
gametophytic 111
gene
  dosage analysis 857
  expression 161, 203, 437, 469, 509, 573, 793, 817
  families 835
  mapping 883
  regulation 527, 867
  transfer 203
genes 745
genetic
  analysis 303
  linkage maps 739
  mapping 493, 857
  mapping software 739
  markers 175
  modification 121
genetics of tissue culture traits 131
germination 691
Gl locus 231
glucan 1, 763
glutamine 315
  synthetase 405
Glycine max 405
glycine-rich proteins 495
glycogen synthase kinase-3 847
GUS 261, 835
  fusion 527

H-box *cis*-element 805
H3 gene 241
hairy-root disease 785
heat-shock cognate protein 143
heavy metal tolerance 309
hexose 315
hierarchy 607
histochemical localization 483
homeostasis 681
Hordeum 887
hydroperoxides 63
hydrotropism 713
hydroxypyruvate 867
hypersensitive response 857, 875
hypervariability 175

IAA conjugates 681
in vitro
  culture 325
  transcription 187
inbred variants 221
indole-3-acetic acid 681
induction 463
integrin 637
intron recognition 393
inverse PCR 191
isozymes 527

jasmonate 887
jasmonic acid 63

late-flowering mutants 231
Lc gene 335
leucine zipper 669
leucine-rich repeat 451
light regulation 161, 437, 793, 867
linkage analysis 739
linked conductance 83
linoleic acid 63
lipid transfer protein 427
localization 415
low temperature stress 309
lycopersicon 131

maize 41, 253, 261, 347, 669
  intron mutant 393
male flower 41
map 745
MAP kinase 611
map-based cloning 493
mechanotransduction 713
Medicago sativa 611, 847
medium 291
merging genetic maps 739
metabolic regulation 325
methionine 721
microisolated chromosomes 883
microspore development 111
microsporogenesis 261
mitochondrial DNA 519
monocot intracellular pathogenesis-related gene wound-responsive promoter 191
morphogenesis 347
moss 51
mRNA stability 221
MsK protein kinases 847
multigene family 545
mutant
  analysis 303
  cell lines 309
  isolation 647
mutants 347
myb 51, 553

N gene 875
nasturtium 691, 701
negative selection 755
Nicotiana 315, 729
  benthamiana 393
  plumbaginifolia 183
nitrate
  assimilation 463
  reductase 315
nitrite reductase 315
nodule development 573
nodulin 573
nuclear protein 563

ocs factor 669
oil body 629
oleosin protein 629
oligosaccharide 415
oligosaccharin 415
organ-specific gene expression 405
overproduction 721
oxidative stress 527

PAL 835
pathogenesis-related proteins 31, 71

PCR 183, 883
  analysis 493
pea 437
pectin 1, 121
peroxisome 867
Petunia 519
  hybrida 553
phase transition 231
phenotypic analysis 303
phenylpropanoid biosynthesis 805
photoperiodic induction 231
photorespiration 867
photosynthesis 817
photosystem II 383
Physcomitrella patens 51
phytochrome 161
Phytophthora parasitica 63
plant
  cell culture 637
  defence 63, 71, 203
  dessication 363
  development 1, 371
  genetics 755
  hormones 371
  MAPs 253
  mitochondria 143
  pathogens 457
  protection 457
  transformation 755
  tubulin 253
plant-pathogen interaction 875
plants 847
plastid
  gene expression 213
  markers 729
  transformation 729
plastocyanin 437
plastome mutations 183
pollen 261
  development 629
polyethylene glycol 729
polygalacturonase 261
polysaccharides 1
positive selection 755
post-transcriptional regulation 335, 537
potassium uptake 647
potato 587, 835
Pro-rich proteins 151
proembryo culture 291
promoter
  analysis 867
  cell division 241
  elements 785
  35S 71
protein
  accumulation 221
  degradation 545
  import 383
  kinase 611, 763
  modification 545
  phosphorylation 143, 451
protoplast 637, 729
Pseudomonas syringae 457
Pytophora parasitica var. *nicotianae* 63

R gene 335
rbcS 817
recombination 493
regeneration capacity, loss of 131
regulatory gene 335
resistance gene 857
RFLP 131, 745
rice 203, 607
RNA
  binding proteins 537
  degradation 213
  fingerprint 887
  polymerase 187
  polymerase I 187
rol genes 371
  rolA 785
  rolB 681
root 607
  culture 131
rRNA gene 187
run-off assay 187

S-locus 451
salicylic acid 71, 563
salt
  stress 637
  tolerance 309
secretion 587
shaggy 847
shoot 607
  regeneration 131
short tandem repeats 175
signal transduction 451
Sinapsis alba 537
sink-regulation 817
Sn gene 335
somatic and germinal excision 773
soybean 175, 405, 573
  nodulins 483
sporophytic 111
SSCP 183
storage protein 221
  gene 883
streptomycin resistance 183
stress 563
  tolerance 309
stretch activation 83
suspensor 291
synchronous culture 213

T4 lysozyme 587
tapetum 41
TAT trinucleotides 175
thermotropism 713
thionin 457, 887
threonine 721
thymidylate biosynthesis 657
tissue specificity 161, 509, 793
tissue-specific factors 509
tobacco 151, 203, 519, 563
  mosaic virus 71, 875
  nuclei 393
tomato fruit development 829

transcription 315, 773
  factors 51, 553, 805
  rates 221
transformation 51
transgenic
  Arabidopsis thaliana 773
  legumes 483
  Lotus 405
  plants 371, 493, 509, 587, 721
  rice 241
  tobacco 437, 681
transglycosylase 701
transmembrane domain 451
transmitting tissue 151
transposon tagging 273, 347, 773
Tropaeolum majus L. 691

ubiquitin conjugating enzyme 545
ubiquitin system 875
ubiquitin-dependent proteolysis 875

variegation 519
Vicia faba 187, 883
virus promoter 619
voltage modulation 83

wheat histone 241
whole-cell extract 187
wound-inducible gene expression 191

xylan 1
xyloglucan 701
  endo-transglycosylase 691

yeast 545

Zea mays L. 325, 527
zein
  mRNAs 325
  proteins 325